REMARKS

SEQUENCE LISTING COMPLIANCE

Applicants supplied paper and CRF copies of the present sequence listing in their response dated February 13, 2002 and again in their response dated April 23, 2002. In the present response, applicants supply a CRF copy of the identical substitute sequence listing in computer-readable format. The content of the sequence listing in paper (previously submitted two times) and computer readable format (attached hereto) is the same and contains no new matter.

The examiner refers to four groups of sequence motifs, and appears to imply that these are not included in the substitute sequence listing. This is not the case. The sequences are identified as follows in the substitute listing:

1)	$PX_n(S/T)GX_3GKGIYFA$	SEQ ID NO:11
	$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$	SEQ ID NO:12
2)	$LLWHG(S/T)X_7IL(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFAX_3SKSAXY$	SEQ ID NO:13
3)	$LX_9NX_2YX_2QLLX(D/E)X_{10/11}WGRVG$	SEQ ID NO:15
	$AX_3FXKX_4KTXNXWX_5FX_3PXK$	SEQ ID NO:16
4)	$QXL(I/L)X_2IX_9MX_{10}PLGKLX_3QIX_6L$	SEQ ID NO:17
	$FYTXIPHXFGX_3PP$	SEQ ID NO:18
	$KX_3LX_2LXDIEXAX_2L$	SEQ ID NO:19

By again supplying the US Patent Office with these copies of the substitute sequence listing, applicants respectfully submit that the application fully complies with the requirements of 37 CFR §§ 1.821-1.825.

ELECTION/RESTRICTION REQUIREMENT

The PCT Administrative Instructions Concerning Unity of Invention instruct the examiner that

> Unity of invention has to be considered in the first place only in relation to the independent claims in an international application and not the dependent claims. ...
>
> (i) If the independent claims avoid the prior art and satisfy the requirement of unity of invention, no problem of lack of unity arises in respect of any claims that depend on the independent claims. In particular, *it does not matter if a dependent claim itself contains a further invention.*

(PCTAI Annex B, Part 1(c).) Presently amended claim 1 is the only independent claim at issue. As amended, this claim is drawn to a PARP homolog having an amino acid sequence comprising a functional NAD^+ binding domain with the sequence $PX_n(S/T)GX_3GKGIYFA$, and lacking any zinc finger motif with the sequence $CX_2CX_MHX_2C$. Such PARP homologs are not known in the prior art. Accordingly, present claim 1 has unity of invention, and all present claims depending from this independent claim also have unity of invention therewith.

Each of the examiner's groups I-XV contain claims dependent on newly amended claim 1, either directly or indirectly. Even if each dependent claim "itself contains a further invention," there is "no problem of lack of unity" (*id.*). Applicants are technically entitled to have all of the present claims examined during the present prosecution, and respectfully request that the examiner proceed to examine all claims on their merits.

However, to further prosecution on the merits, and with a view to PCT Rule 13.4,

which qualifies the number of dependent claims to that which is "reasonable," applicants respectfully request that the examiner consider at least the following claim groupings together in the present prosecution:

Group I	Claims 1-4, drawn to the novel PARP homologs;
Group V	Claims 6-10, drawn to nucleotide sequences encoding these PARP homologs, expression cassettes, vectors and recombinant microorganisms;
Group VI	Claim 11, drawn to a transgenic mammal comprising a recombinant vector with a nucleotide sequence encoding the novel PARP homologs;
Group VII	Claim 12, drawn to PARP-deficient eukaryotic cell or mammal;
Group XIII	Claim 29, drawn to a gene therapy composition using antisense technology against the novel PARP homologs; and
Group XIV	Claim 30, drawn to a pharmaceutical composition comprising the novel PARP homologs.

The claims so grouped are conceptually integrated as corresponding protein and DNA sequences, and products employing these sequences. Applicants respectfully request that the examiner consider at least these claim groupings together in the present examination.

Applicants provisionally elect Group I, with traversal and request for reconsideration as indicated above.

The examiner indicates three groupings of partial sequence motifs, indicating that they are separate inventions. Applicants are instructed to elect a single group and a single sequence for examination. However, those sequences in grouping 1) are progressively longer iterations of the NAD^+ binding domain of the novel PARP homologs. This can be seen by lining up each of the part-sequence motifs as follows:

1) **$PX_n(S/T)GX_3GKGIYFA$**
*(S/T)XGLR(I/V)X***$PX_n(S/T)GX_3GKGIYFA$**
LLWHG(S/T)X_7IL*(S/T)XGLR(I/V)X***$PX_n(S/T)GX_3GKGIYFAX_3$**SKSAXY

Further, each of the part-sequence motifs of group 2) is an additional N-terminal motif that is optionally present in the novel PARP homolog. None of the part-sequence motifs of groups 1) and 2) is an independent PARP homolog sequence according to the present invention. Accordingly, none of these can correctly be the subject of a species election requirement.

Applicants provisionally elect SEQ ID NO:2 of group 3), but reassert that unity of invention is present among all claims, and further remind the examiner that 37 CFR §1.146 is not applicable to PCT applications. Unity of invention clearly exists between these sequences, as each contains or codes for a sequence having the part-sequence motif $PX_n(S/T)GX_3GKGIYFA$, and not having the part-sequence zinc-finger motif $CX_2CX_MHX_2C$. Therefore, each contains or codes for this special technical feature as required by PCT Rule 13.1 and 37 CFR §1.475. Applicants respectfully request that all sequences of group 3) be examined in the present prosecution.

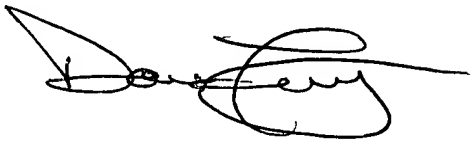
CONCLUSION

In view of the foregoing amendments and remarks, applicants consider that the rejections of record have been obviated and respectfully solicit passage of the application to issue.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit

any excess fees to such deposit account.

Respectfully submitted,
KEIL & WEINKAUF



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS

Please amend claims 1 and 2 to read as follows:

1. A poly(ADP-ribose) polymerase (PARP) homolog and the functional equivalents thereof having [which has] an amino acid sequence which has

a) a functional NAD^+ binding domain

and

b) no zinc finger sequence motif of the general formula

$CX_2CX_MHX_2C$ (SEQ ID NO:30)

in which

m is an integral value of [from] 28 or 30, and the X radicals are,

independently of one another, any amino acid;

and wherein the functional NAD^+ binding domain comprises the sequence motif $PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11) in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid [the functional equivalents thereof].

2. A PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises one of the following general sequence motifs:

[$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11),]

(S/T)XGLR(I/V)XPX$_n$(S/T)GX$_3$GKGIYFA (SEQ ID NO:12) or

LLWHG(S/T)X$_7$IL(S/T)XGLR(I/V)XPX$_n$(S/T)GX$_3$GKGIYFAX$_3$SKSAXY (SEQ ID NO:13)

in which

n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.